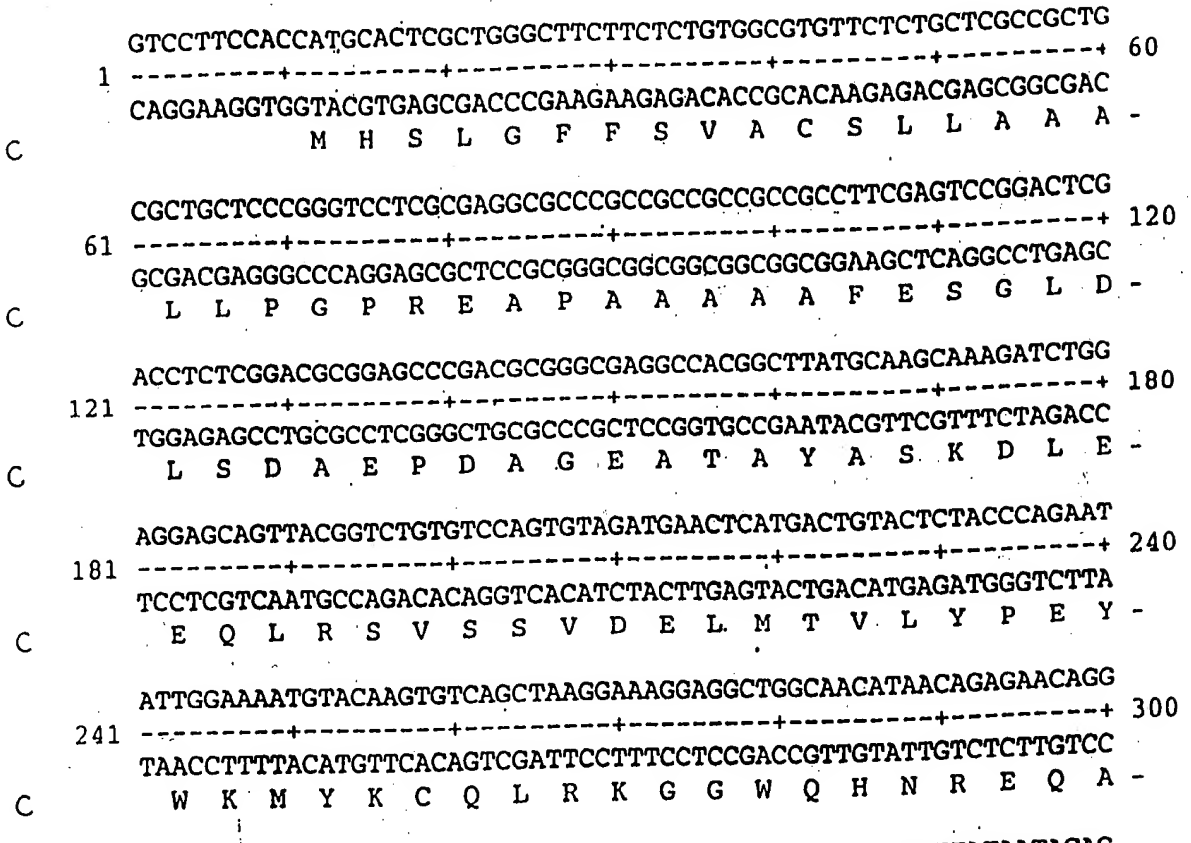
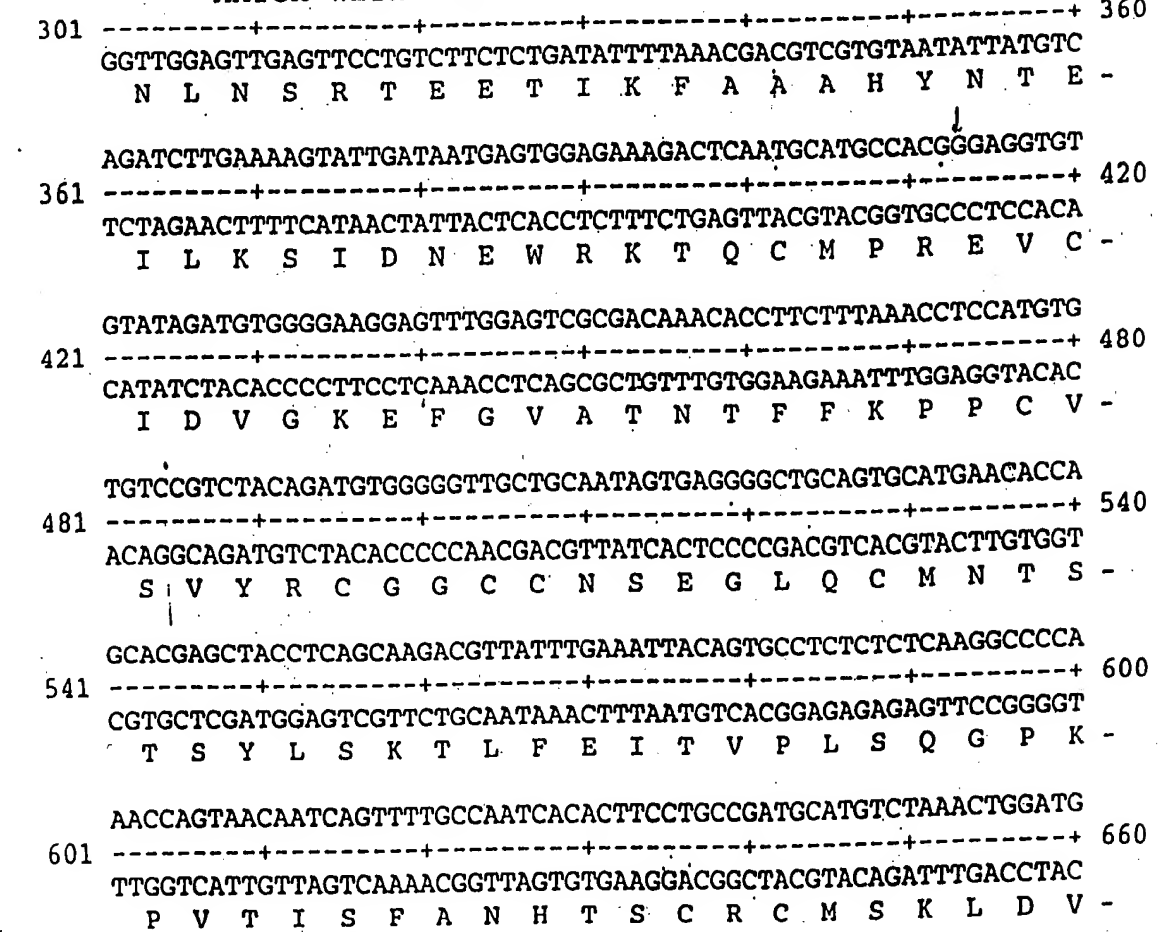
FIG. 1A



MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

FIG. 1B



MATCH WITH FIG. 1C

MATCH WITH FIG. 1B

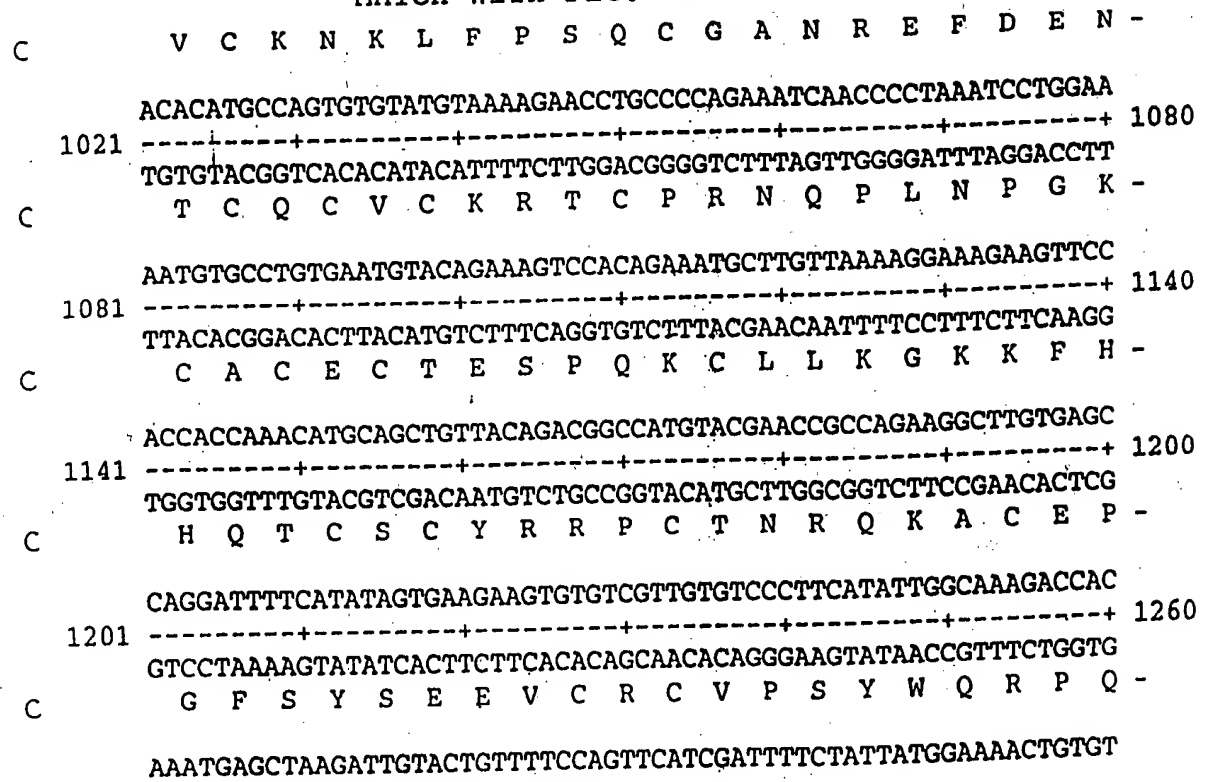
FIG. 1C

```
                TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
          661   ---------+---------+---------+---------+---------+---------+  720
                AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAG
          C       Y  R  Q  V  H  S  I  I  R  R  S  L  P  A  T  L  P  Q  C  Q  -

                AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
          721   ---------+---------+---------+---------+---------+---------+  780
                TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
          C       A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L  -

                TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
          781   ---------+---------+---------+---------+---------+---------+  840
                ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
          C       A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H  -

                ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
          841   ---------+---------+---------+---------+---------+---------+  900
                TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
          C       D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A  -

                CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
          901   ---------+---------+---------+---------+---------+---------+  960
                GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCA
          C       G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C  -

                GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
          961   ---------+---------+---------+---------+---------+---------+ 1020
                CACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

MATCH WITH FIG. 1D

FIG. 1D

MATCH WITH FIG. 1C



MATCH WITH FIG. 1E

MATCH WITH FIG. 1D

FIG. 1E

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
C     M  S  *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAAA
1621 ---------+---------+---------+---------+---------+---- 1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTTT
```

```
  1  CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
     ---------+---------+---------+---------+---------+---------+
                M  T  V  L  Y  P  E  Y  W  K  M  Y  K  C  Q  L  R

 71  AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAAATGTACAAGTGTCAGCTAAG
     ---------+---------+---------+---------+---------+---------+
      K  G  G  W  Q  H  N  R  E  Q  A  N  L  N  S  R  T  E  E  T

121  GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
     ---------+---------+---------+---------+---------+---------+
      I  K  F  A  A  A  H  Y  N  T  E  I  L  K  S  I  D  N  E  W

181  TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
     ---------+---------+---------+---------+---------+---------+
      R  K  T  Q  C  M  P  R  E  V  C  I  D  V  G  K  E  F  G  V

241  GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
     ---------+---------+---------+---------+---------+---------+
      A  T  N  T  F  F  K  P  P  C  V  S  V  Y  R  C  G  G  C  C

301  CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG
     ---------+---------+---------+---------+---------+---------+
```

FIG. 2A

```
361  CAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATT
     ---------+---------+---------+---------+---------+---------+
      N  S  E  G  L  Q  C  M  N  T  S  T  S  Y  L  S  K  T  L  F

421  TGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCA
     ---------+---------+---------+---------+---------+---------+
      E  I  T  V  P  L  S  Q  G  P  K  P  V  T  I  S  F  A  N  H

481  CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
     ---------+---------+---------+---------+---------+---------+
      T  S  C  R  C  M  S  K  L  D  V  Y  R  Q  V  H  S  I  I  R

541  ACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAA
     ---------+---------+---------+---------+---------+---------+
      R  S  L  P  A  T  L  P  Q  C  Q  A  A  N  K  T  C  P  T  N

601  TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTC
     ---------+---------+---------+---------+---------+---------+
      Y  M  W  N  N  H  I  C  R  C  L  A  Q  E  D  F  M  F  S  S

661  GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
     ---------+---------+---------+---------+---------+---------+
      D  A  G  D  D  S  T  D  G  F  H  D  I  C  G  P  N  K  E  L
```

FIG.2B

```
721  GGATGAAGAGACCTGTCAGTGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC
     ---------+---------+---------+---------+---------+---------+
      D  E  E  T  C  Q  C  V  C  R  A  G  L  R  P  A  S  C  G  P

781  CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAACTCTTCCCCAG
     ---------+---------+---------+---------+---------+---------+
      H  K  E  L  D  R  N  S  C  Q  C  V  C  K  N  K  L  F  P  S

841  CCAATGTGGGGCCAACCGAGAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAAC
     ---------+---------+---------+---------+---------+---------+
      Q  C  G  A  N  R  E  F  D  E  N  T  C  Q  C  V  C  K  R  T

901  CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC
     ---------+---------+---------+---------+---------+---------+
      C  P  R  N  Q  P  L  N  P  G  K  C  A  C  E  C  T  E  S  P

961  ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACG
     ---------+---------+---------+---------+---------+---------+
      Q  K  C  L  L  K  G  K  K  F  H  H  Q  T  C  S  C  Y  R  R

1021 GCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
     ---------+---------+---------+---------+---------+---------+
      P  C  T  N  R  Q  K  A  C  E  P  G  F  S  Y  S  E  E  V  C
```

FIG. 2C

```
1081  TCGTTGTGTCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTTCCA
      ---------+---------+---------+---------+---------+---------+
       R  C  V  P  S  Y  W  Q  R  P  Q  M  S

1141  GTTCATCGATTTTCTATTATGGAAAACTGTGTTGCCACAGTAGAACTGTCTGTGAACAGA
      ---------+---------+---------+---------+---------+---------+

1201  GAGACCCTTGTGGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTCCTGAACCATGTGGA
      ---------+---------+---------+---------+---------+---------+

1261  TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCTCTTGTAAAGACTGGTTTT
      ---------+---------+---------+---------+---------+---------+

1321  CTGCCAATGACCAAACAGCCAAGATTTTCCTCTTGTGATTTCTTTAAAAGAATGACTATA
      ---------+---------+---------+---------+---------+---------+

1381  TAATTTATTTCCACTAAAAATATTGTTTCTGCATTCATTTTTATAGCAACAACAATTGGT
      ---------+---------+---------+---------+---------+---------+

1441  AAAACTCACTGTGATCAATATTTTTATATCATGCAAAATATGTTTAAAATAAAATGAAAA
      ---------+---------+---------+---------+---------+---------+

1501  TTGTATTATAAAAAAAAAAAAAAA
      ---------+---------+------
```

FIG. 2D

```
        1                                                  50
Pdgfa   .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb   MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf   .....MNFLL SWVHWSLALL LY........ .......... .LHHAKWSQA
Vegf2   .......MTV LYPEYWKMYK CQ........ .......... .LRKGGWQHN

        51                                                100
Pdgfa   IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb   GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf   APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... ..........
Vegf2   REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... ..........

        101                                               150
Pdgfa   AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb   AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf   SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2   TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

        151                                               200
Pdgfa   RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.... AT........
Pdgfb   QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKC.... ETVAAARPVT
 Vegf   EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2   STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

FIG. 3A

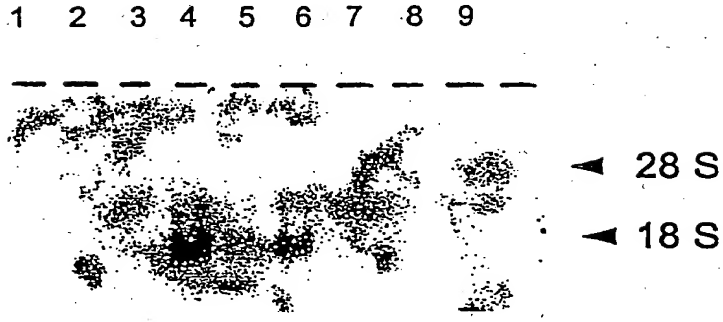
```
        201                                                  250
Pdgfa   ....TSLNPD YREEDTDVR. .......... .......... ..........
Pdgfb   RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf   RGK........ .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2   RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG

        251                                                  300
Pdgfa   .......... .......... .......... .......... ..........
Pdgfb   A......... .......... .......... .......... ..........
 Vegf   ....CGP... .......... .......CSE RRKHLFVQDP QTCKCSCKNT
Vegf2   FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

        301                                                  350
Pdgfa   .......... .......... .......... .......... ..........
Pdgfb   .......... .......... .......... .......... ..........
 Vegf   ..DSRCKARQ LELNERTCRC DKPRR..... .......... ..........
Vegf2   LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL

        351                                                  398
Pdgfa   .......... .......... .......... .......... .........
Pdgfb   .......... .......... .......... .......... .........
 Vegf   .......... .......... .......... .......... .........
Vegf2   KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLWING TABLE				
	PDGFα	PDGFβ	VEGF	VEGF2
PDGFα				
PDGFβ	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

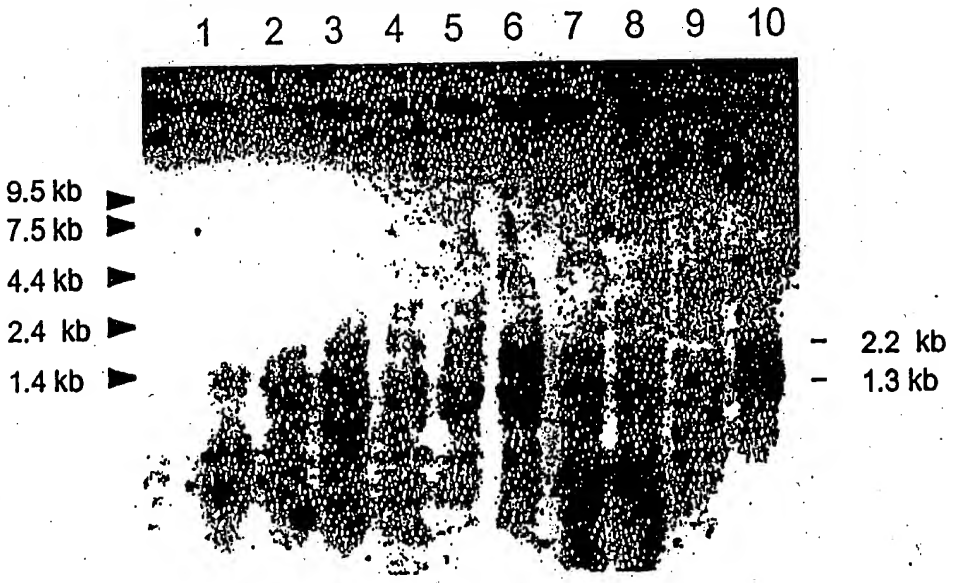
FIG. 4

Expression of VEGF2 mRNA in
Human Breast Tumor Cells



1. normal breast tissue
2. breast tumor tissue
3-9. breast tumor cell lines.

FIG. 5

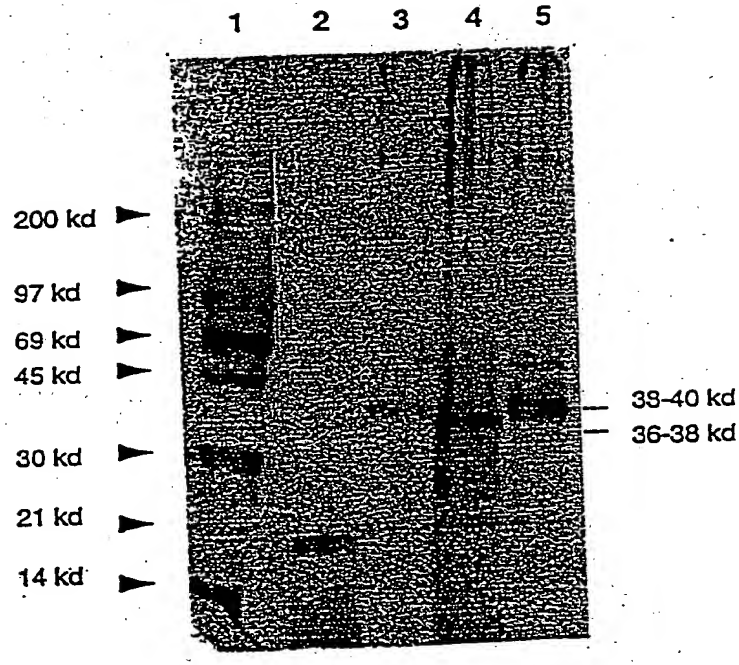


1.	ovary	6.	lung
2.	testes	7.	spleen
3.	gall bladder	8.	prostate
4.	kidney	9.	Hippocampus
5.	liver	10.	heart

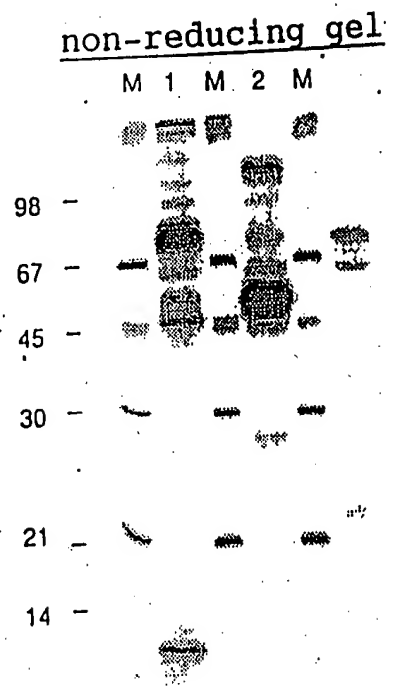
Expression of VEGF2 mRNA in human adult tissues.

FIG. 6

FIG. 7

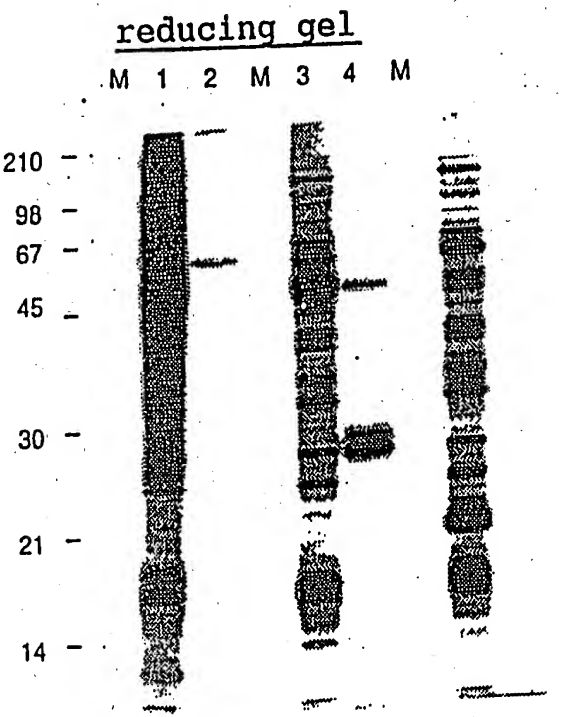


Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse & forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)



Lane M: Marker
Lane 1: vector medium
Lane 2: VEGF2 medium

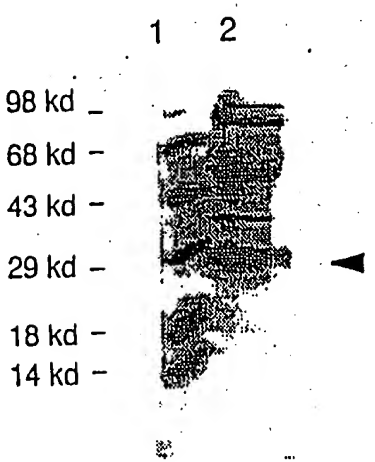
FIG. 8A



Lane M: Marker
Lane 1: vector cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 cytoplasm
Lane 4: VEGF2 medium

FIG. 8B

FIG. 9



Lane 1: Molelular weight marker
Lane 2. Precipitates containing VEGF2.

FIG. 10

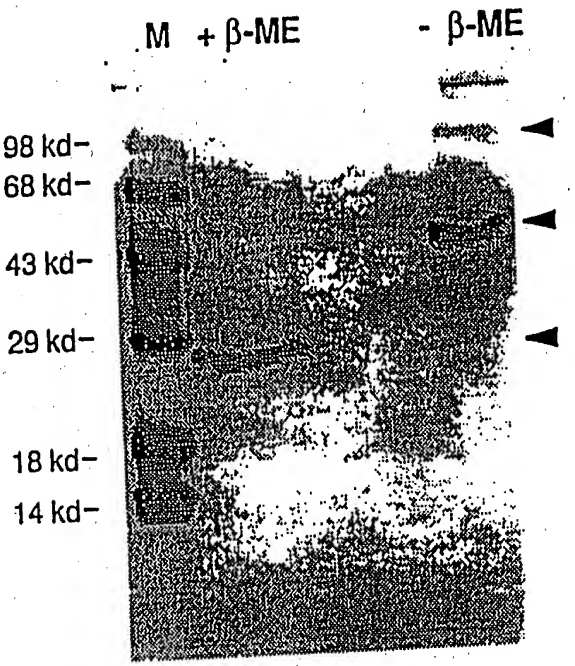


FIG. 11

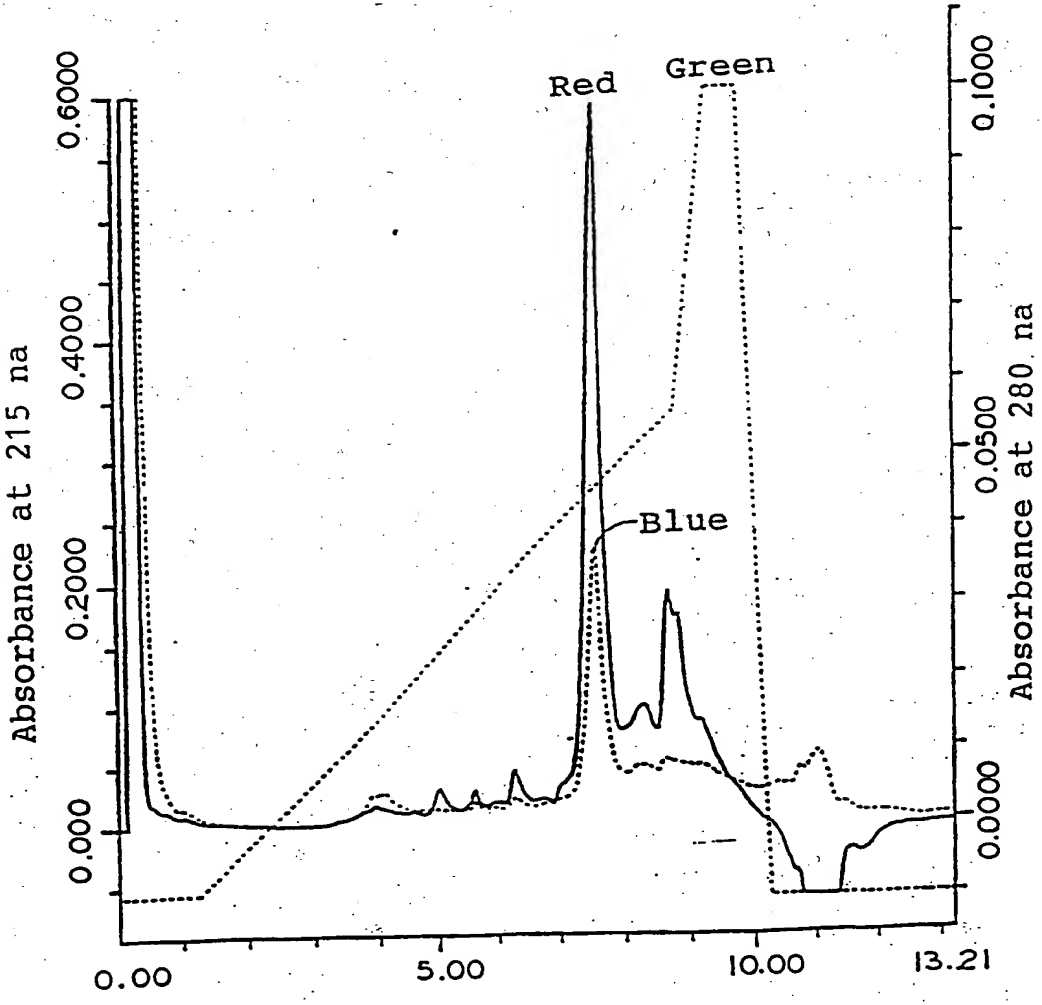

Red
Green
Blue
Absorbance at 215 na
0.6000
0.4000
0.2000
0.000
Absorbance at 280 na
0.1000
0.0500
0.0000
0.00
5.00
10.00
13.21

FIG. 12

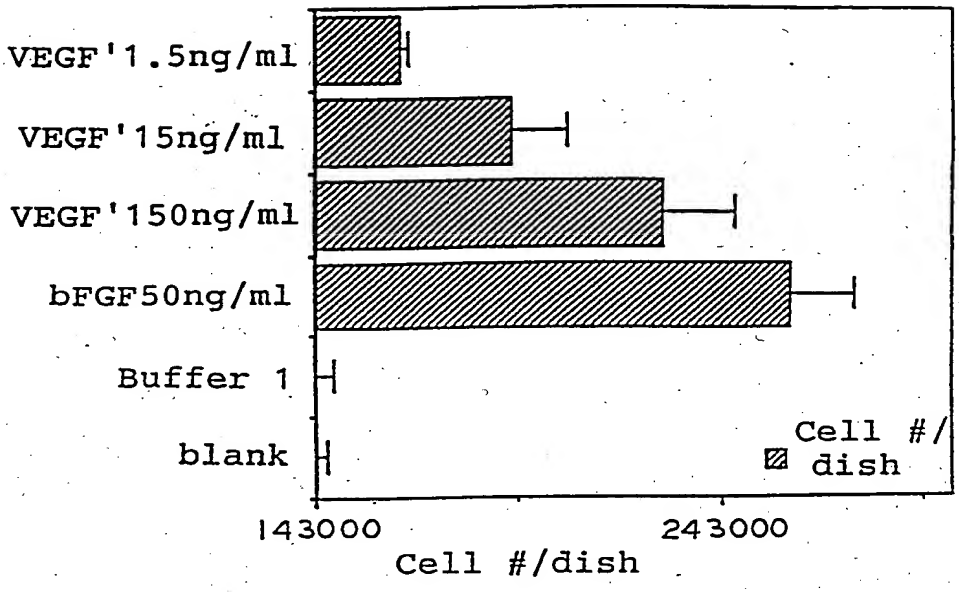
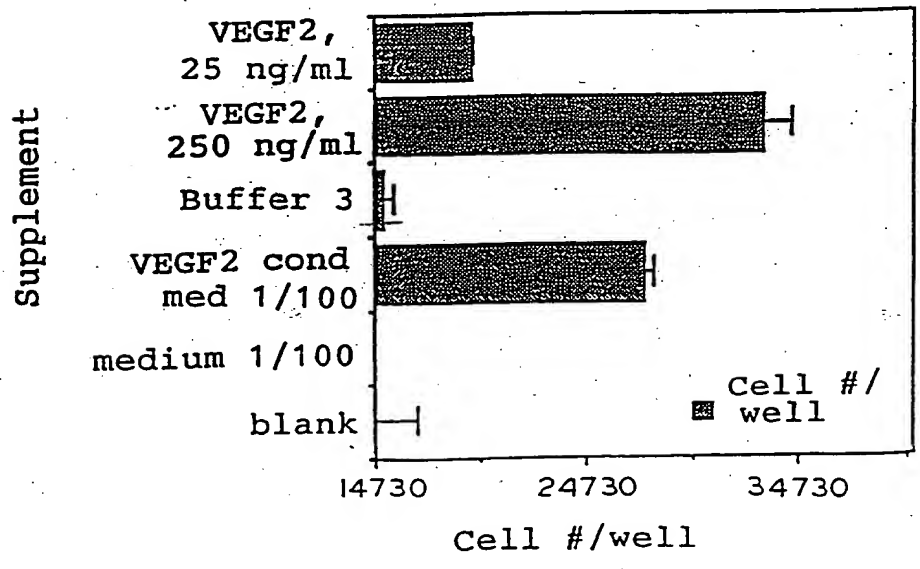


FIG. 13



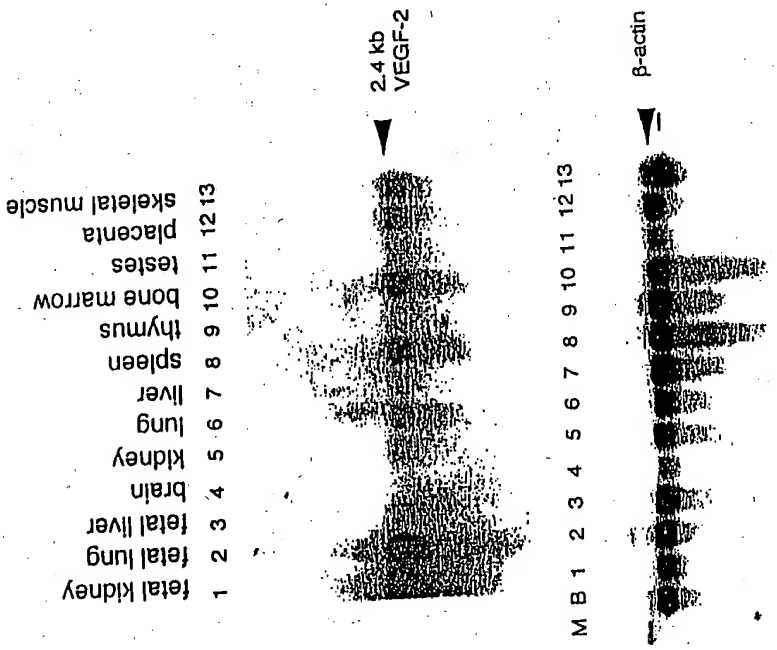
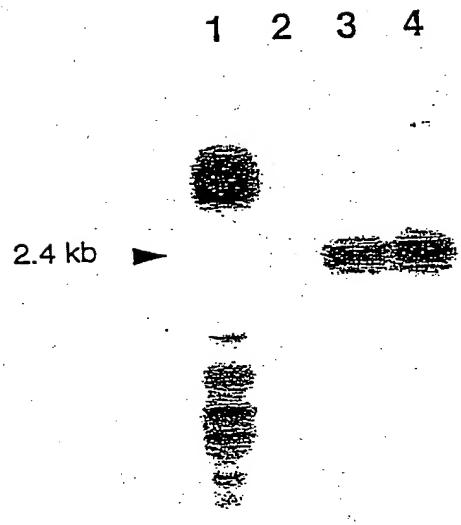


Figure 14



1. Molecular Weight Marker
2. umbelical vein endothelial cells
3. aortic smooth muscle cells
4. Dermal fibroblast

Figure 15

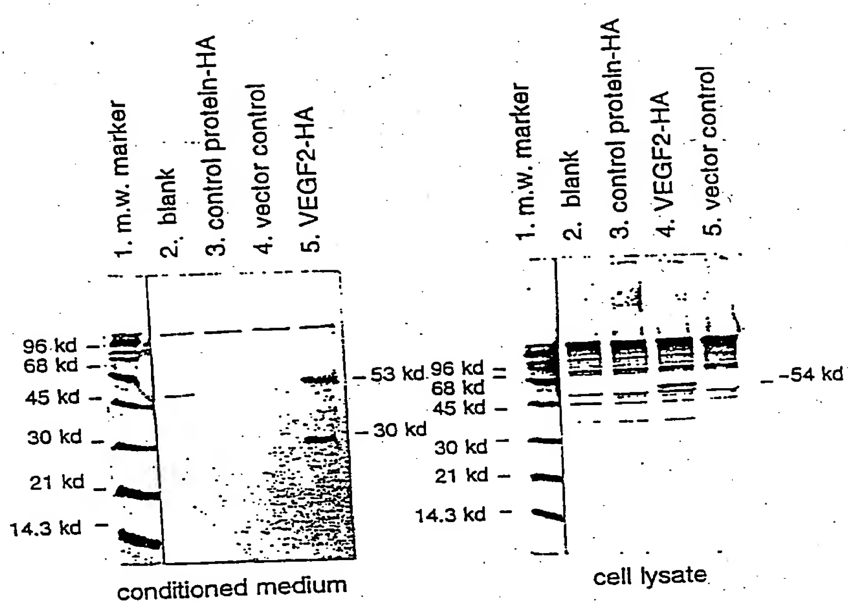

1. m.w. marker
2. blank
3. control protein-HA
4. vector control
5. VEGF2-HA
96 kd
68 kd
45 kd
30 kd
21 kd
14.3 kd
53 kd
30 kd
conditioned medium
1. m.w. marker
2. blank
3. control protein-HA
4. VEGF2-HA
5. vector control
96 kd
68 kd
45 kd
30 kd
21 kd
14.3 kd
54 kd
cell lysate

Figure 16

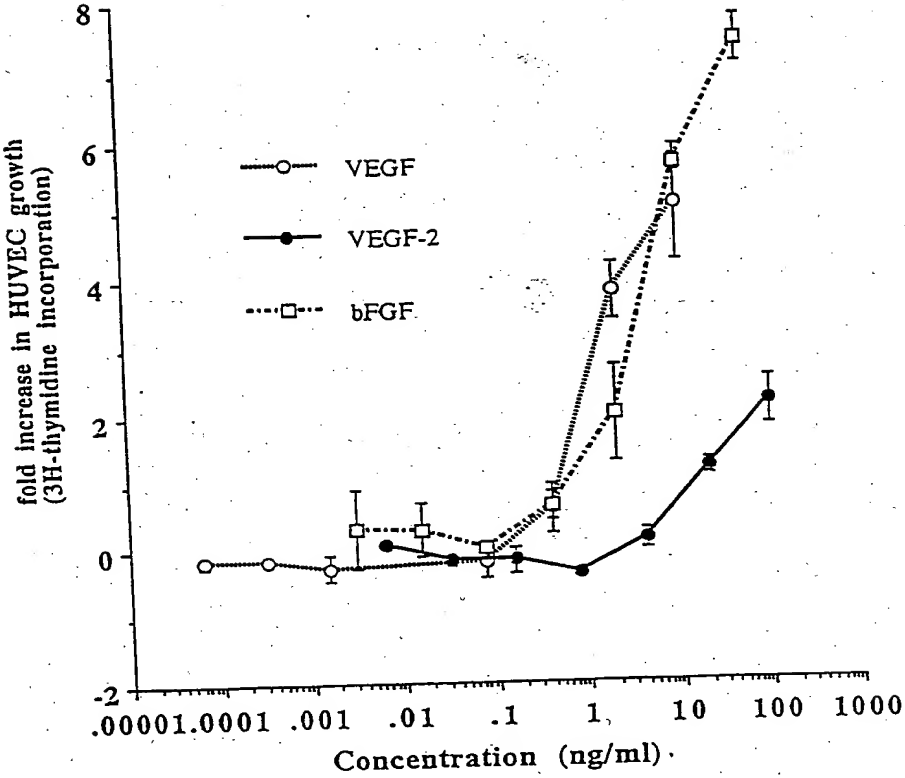


Figure 17

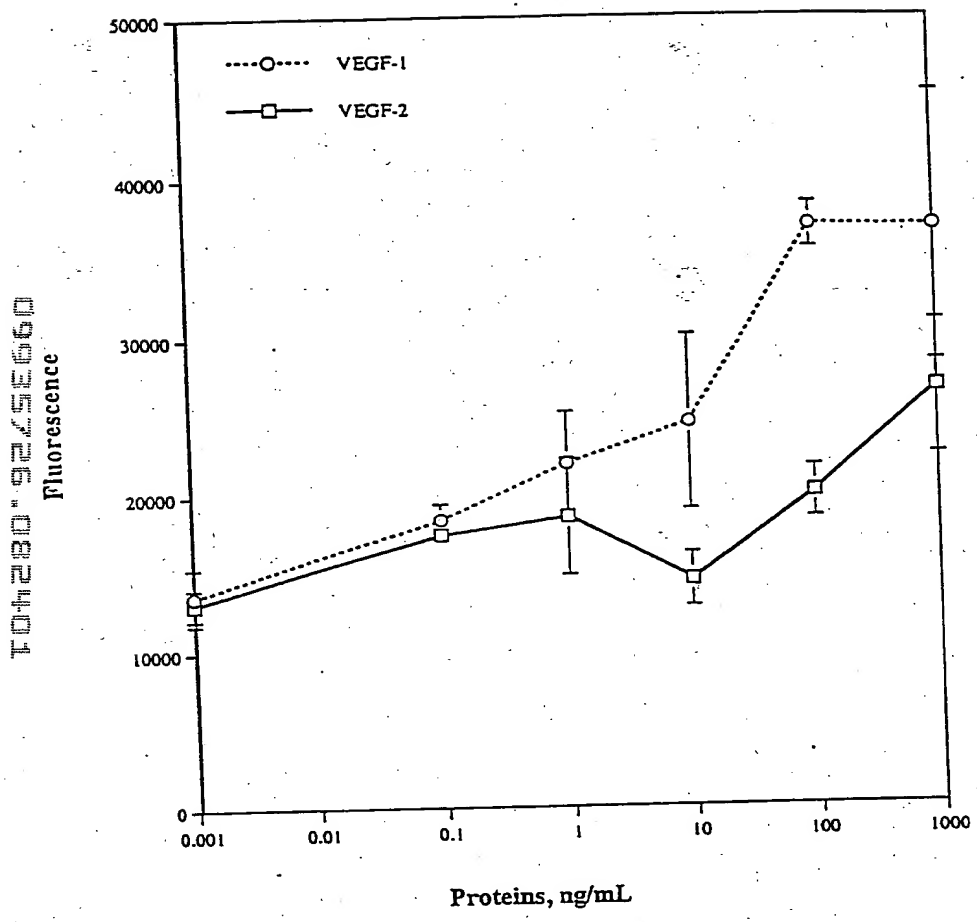

VEGF-1
VEGF-2
50000
40000
30000
20000
10000
0
Fluorescence
0.001
0.01
0.1
1
10
100
1000
Proteins, ng/mL

Figure 18

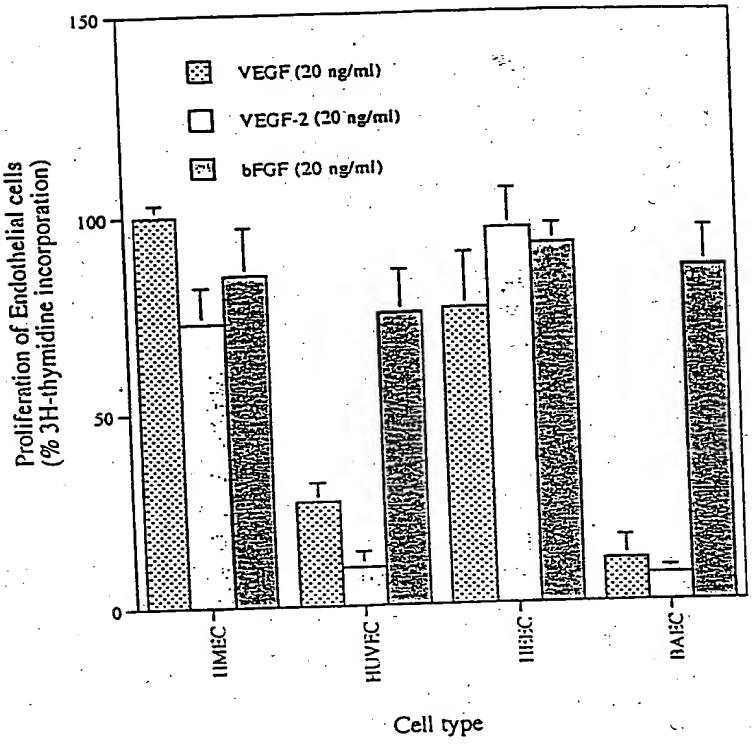


Figure 19

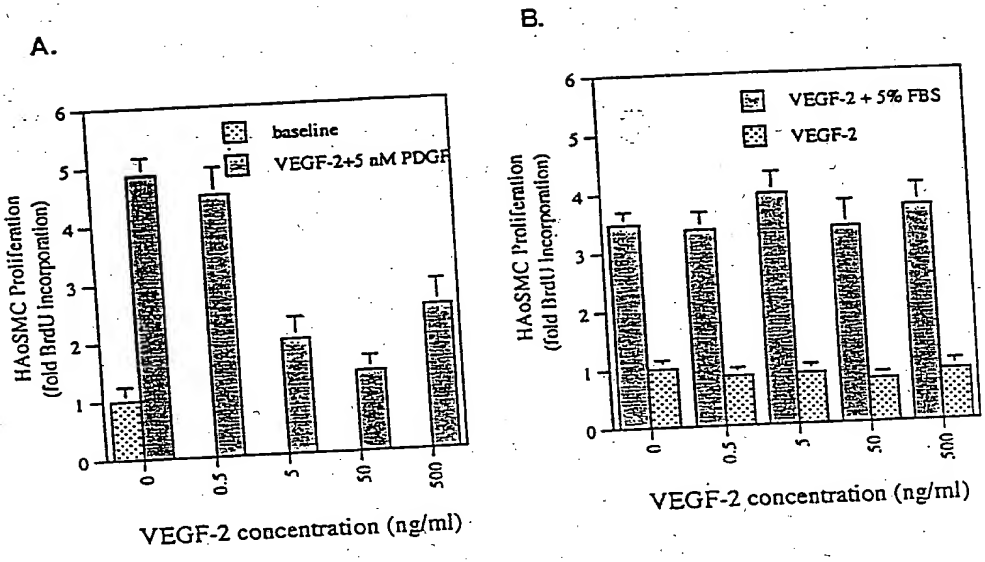

A.
HAoSMC Proliferation
(fold BrdU Incorporation)
baseline
VEGF-2+5 nM PDGF
VEGF-2 concentration (ng/ml)
B.
HAoSMC Proliferation
(fold BrdU Incorporation)
VEGF-2 + 5% FBS
VEGF-2
VEGF-2 concentration (ng/ml)

Figure 20

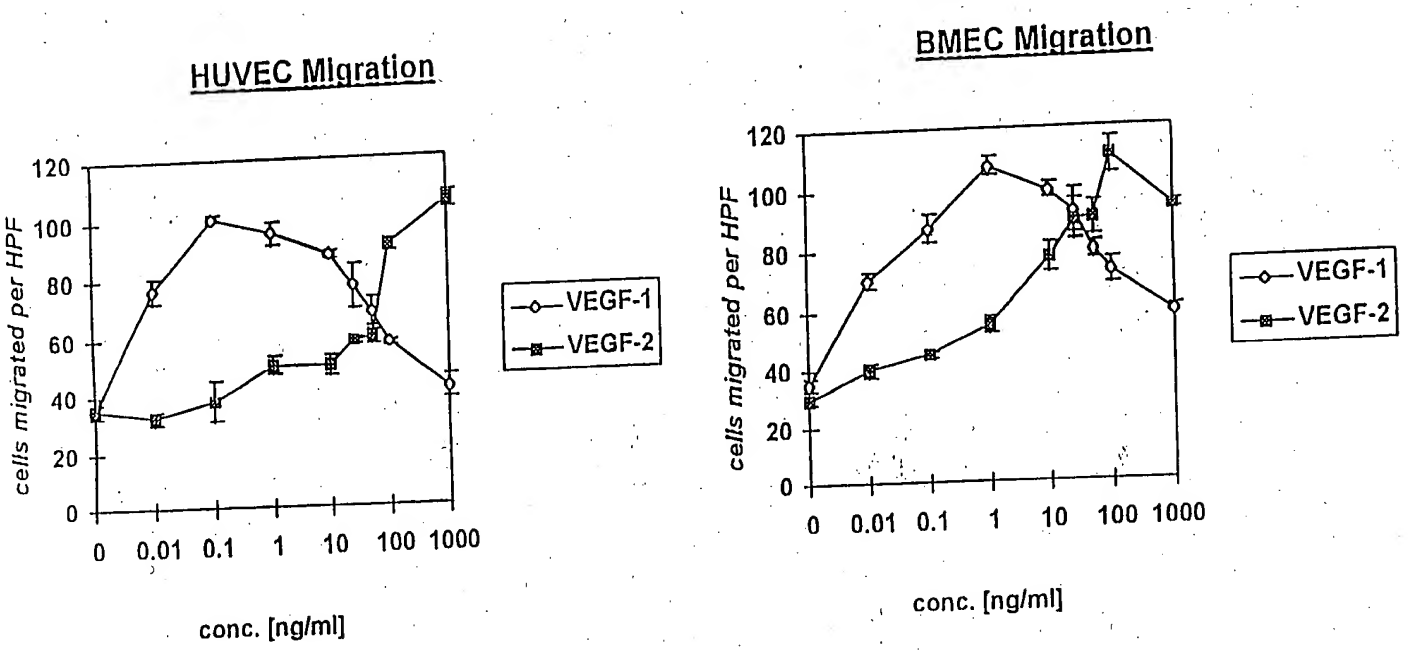


Figure 21

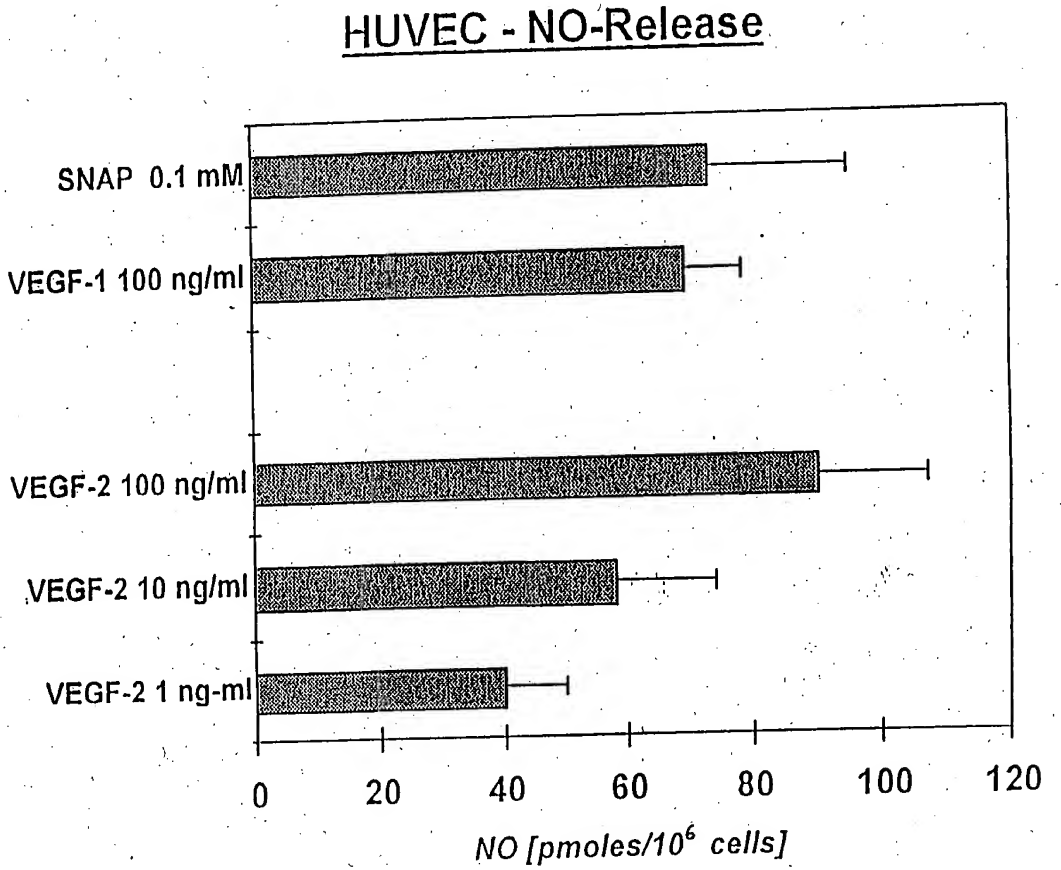
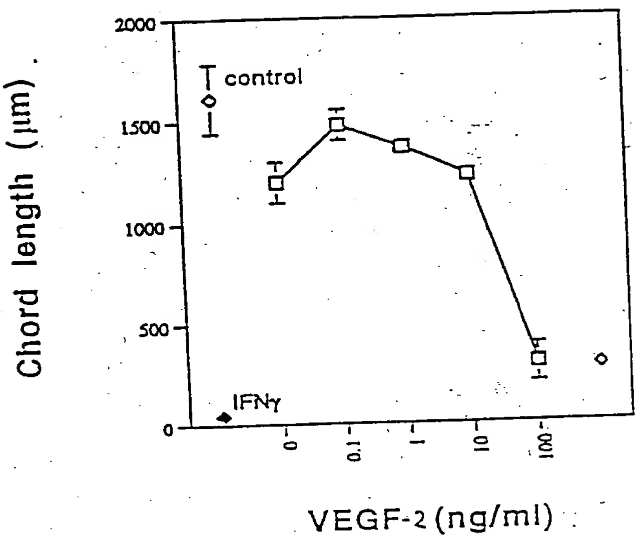


Figure 22



Chord length (μm)
2000
1500
1000
500
0
control
IFNγ
0
0.1
1
10
100
VEGF-2 (ng/ml)

Figure 23

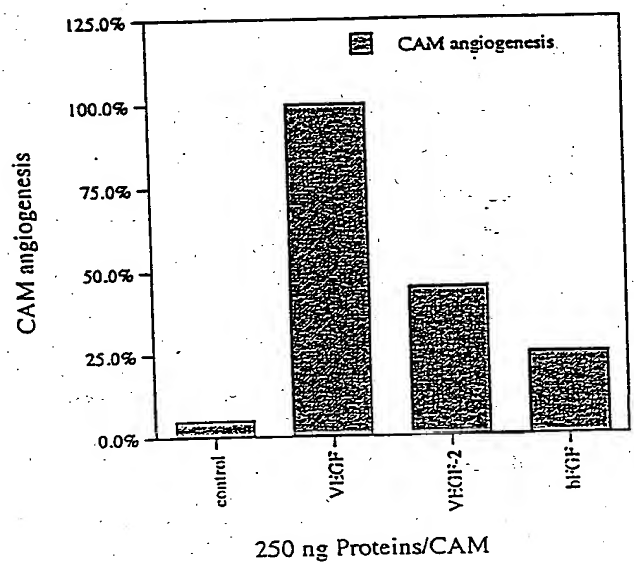
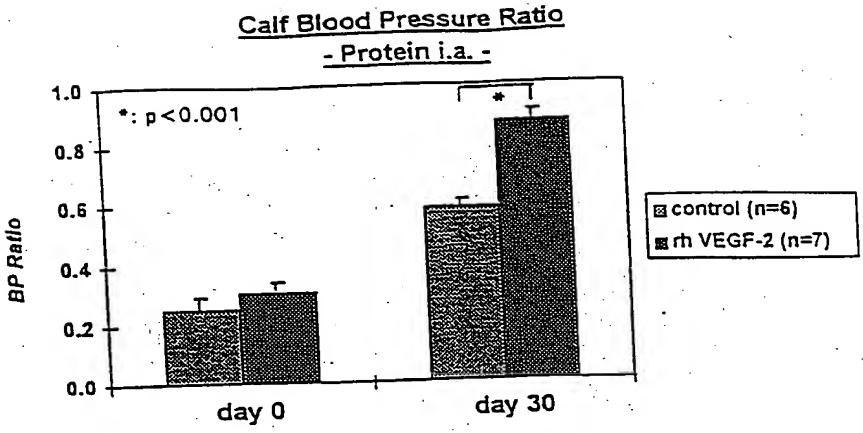
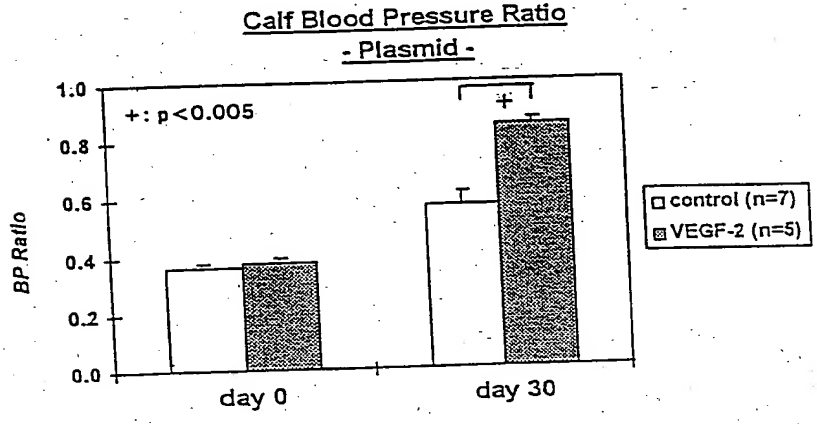


Figure 24





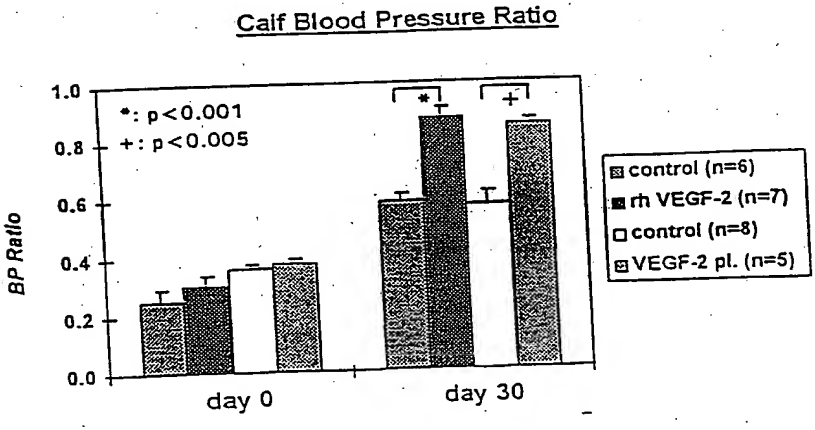


Figure 25A

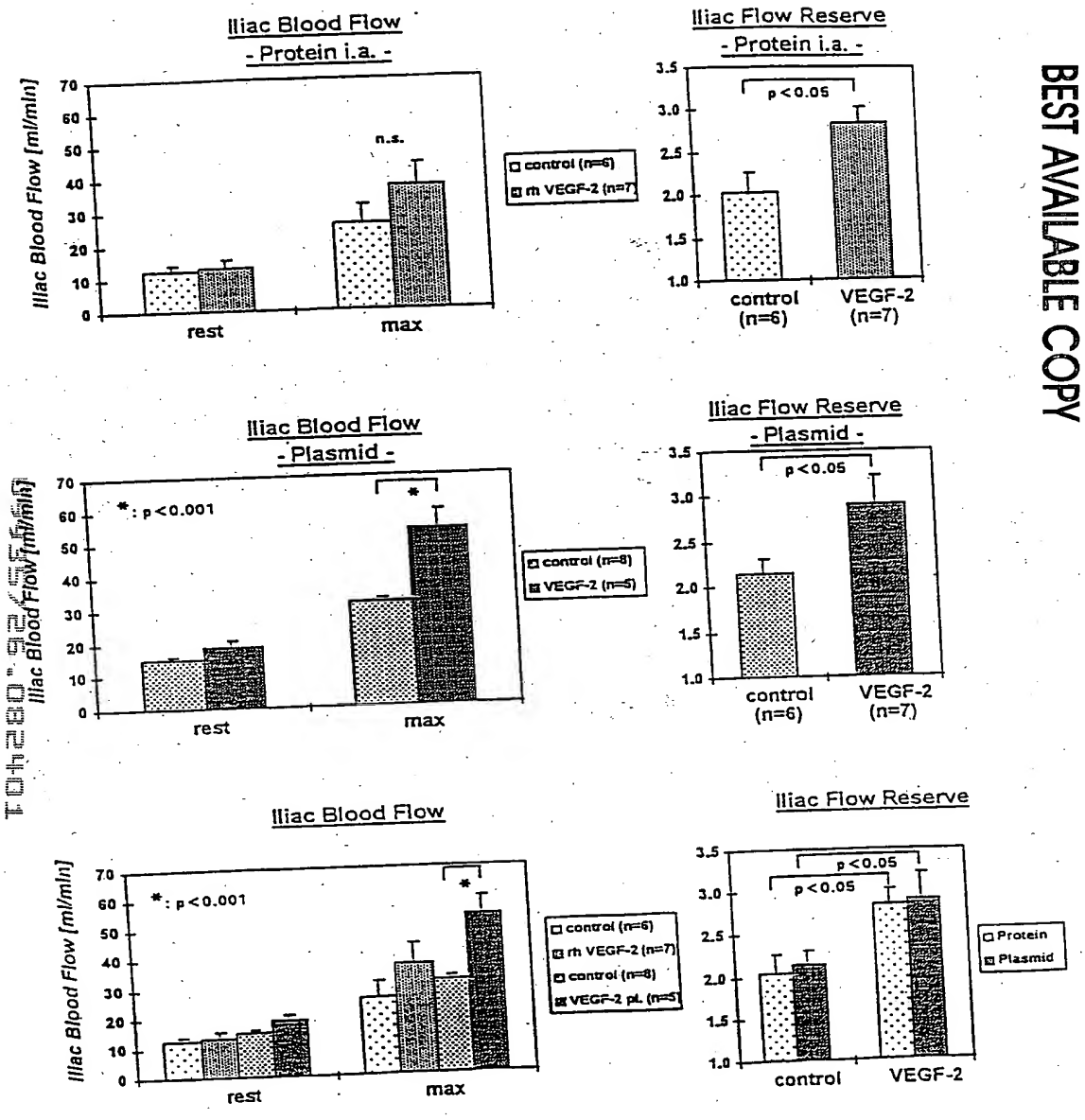


Figure 25B

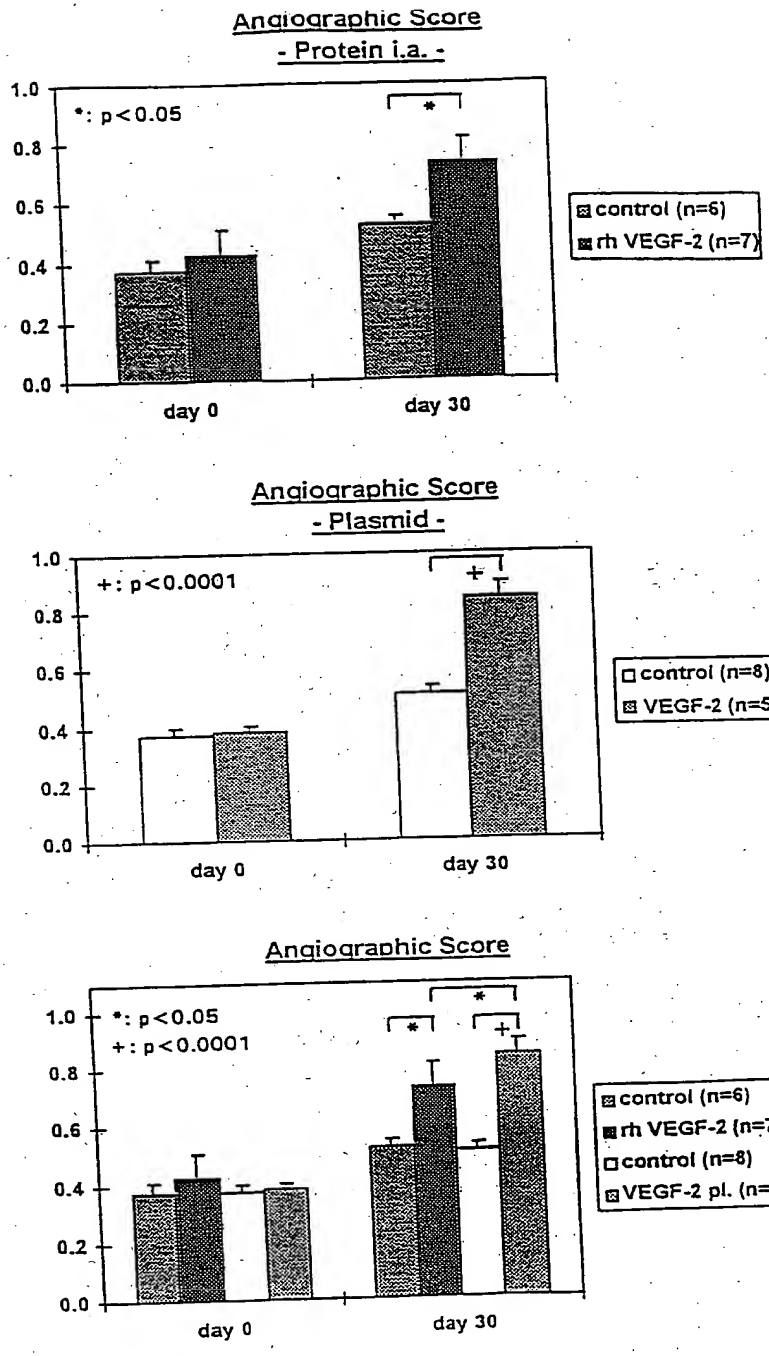
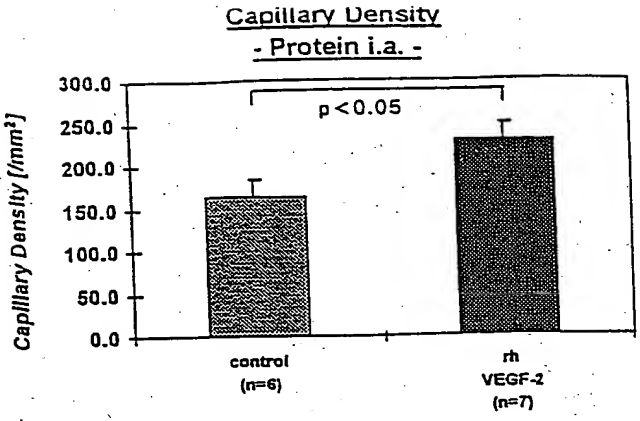
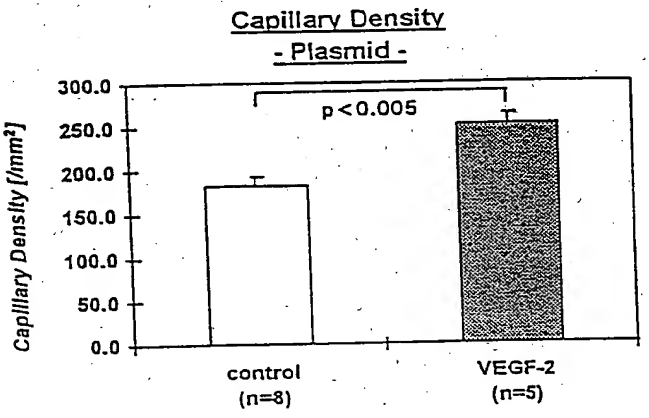

Angiographic Score
- Protein i.a. -
*: p<0.05
control (n=6)
rh VEGF-2 (n=7)
day 0
day 30
Angiographic Score
- Plasmid -
+: p<0.0001
control (n=8)
VEGF-2 (n=5)
day 0
day 30
Angiographic Score
*: p<0.05
+: p<0.0001
control (n=6)
rh VEGF-2 (n=7)
control (n=8)
VEGF-2 pl. (n=5)
day 0
day 30

Figure 25C





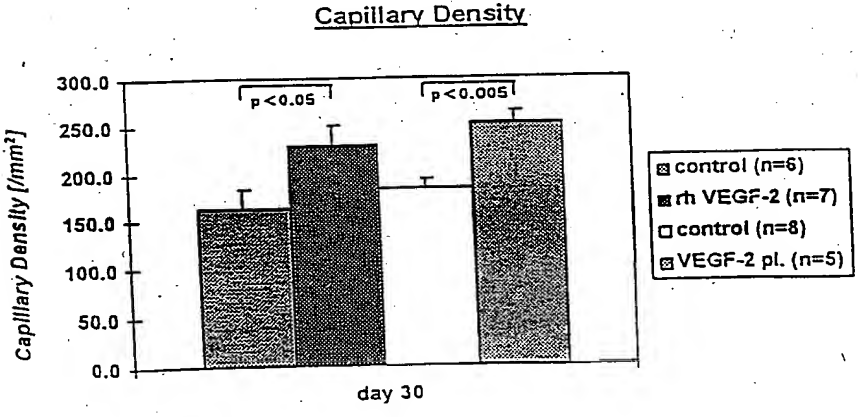


Figure 25D

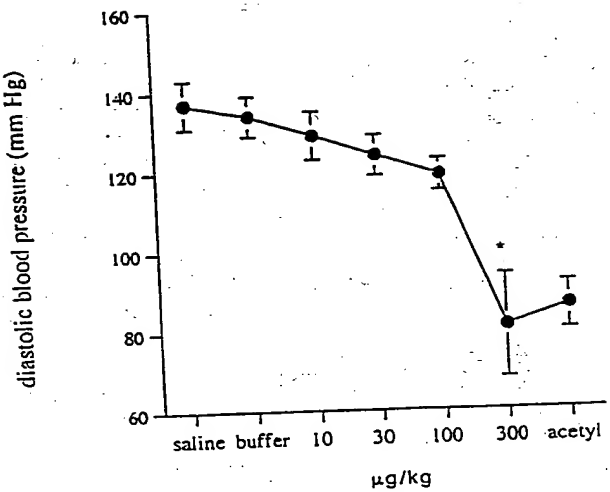

160
140
120
100
80
60
diastolic blood pressure (mm Hg)
saline
buffer
10
30
100
300
acetyl
µg/kg
*

Figure 26A

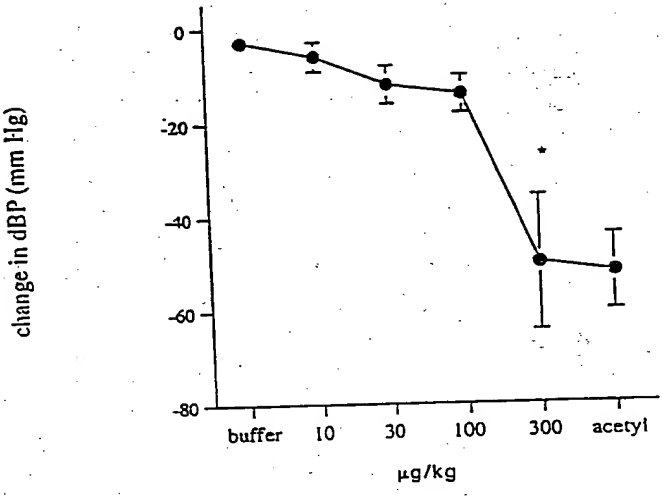


Figure 26B

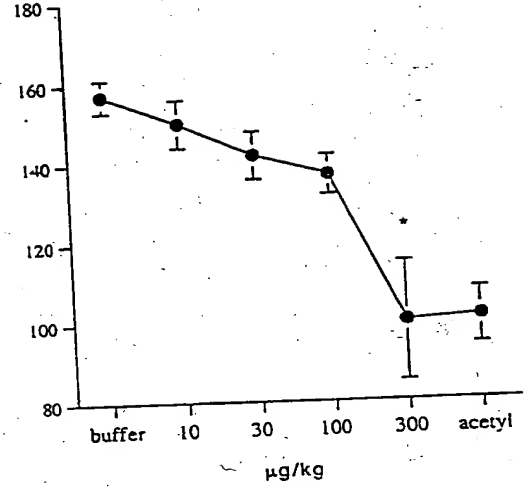


Figure 26C

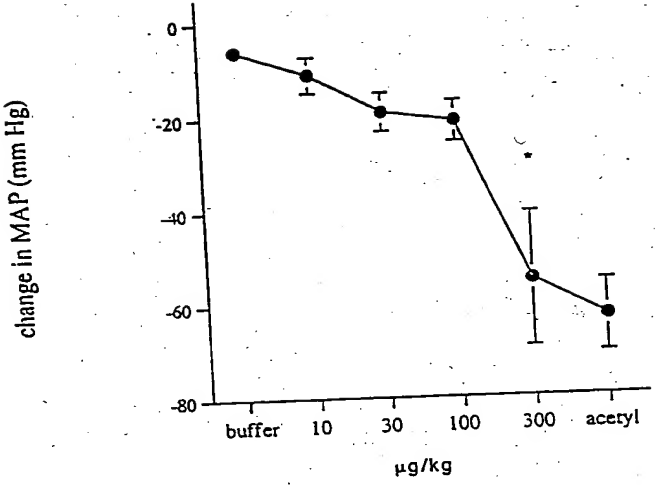
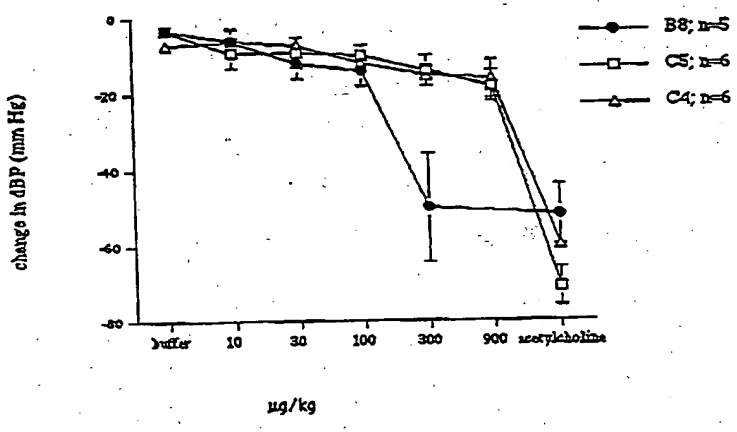


Figure 26D

Change in diastolic blood pressure of SHR rats given increasing doses of VEGF-2

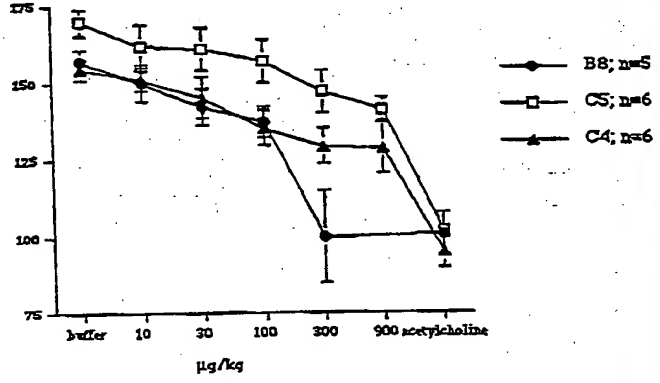


Increasing doses of VEGF-2 (HG00403-B8, HG00404-C5, and HG00404-C4) were administered to 13-14 week old SHR (spontaneously hypertensive rats) and the data are expressed as the mean +/- SEM. Statistical analysis was performed with a paired t-test and significance was defined as $p < 0.05$ vs. the response to buffer alone. The response to B8 and C4 were significant at the 300 µg/kg dose. The response to C5 was significant at the 100, 300, and 900 µg/kg doses.

The effect of increasing doses of VEGF-2 on the mean arterial pressure (MAP) of SHR rats

Figure 26E

The effect of increasing doses of VEGF-2 on the mean arterial pressure (MAP) of SHR rats

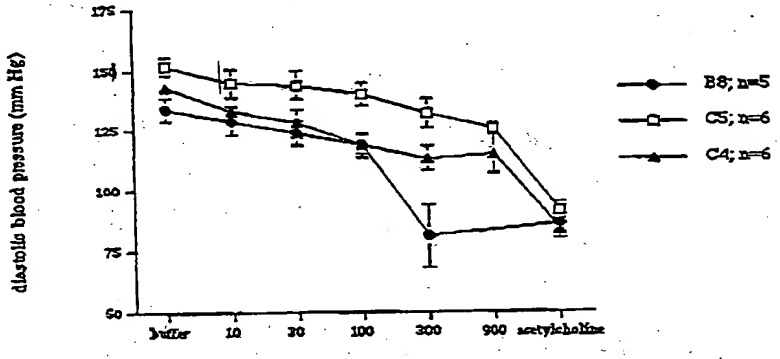


Increasing doses of VEGF-2 (HG00403-B8, HG00404-C5, and HG00404-C4) were administered to 13-14 week old SHR (spontaneously hypertensive rats) and the data are expressed as the mean +/- SEM. Statistical analysis was performed with a paired t-test and significance defined as $p < 0.05$ vs. the response to buffer alone. The response to B8 was significant at a 300µg/kg dose. Administration of C5 yielded significant responses at doses greater than or equal to 100 µg/kg. The response to C4 was significant when 10, 100, 300, and 900 ng/kg were given.

The effect of VEGF-2 on the diastolic blood pressure of SHR rats

Figure 26F

The effect of VEGF-2 on the diastolic blood pressure of SHR rats



Increasing doses of VEGF-2 (HG00403-B8, HG00404-C5, HG00404-C4) were administered to 13-14 week old SHR (spontaneously hypertensive rats) and the data are expressed as the mean +/- SEM. Statistical analysis was performed with a paired t-test and statistical significance was defined as $p < 0.05$ vs. the response to buffer alone. The response to B8 was significant only at the 300 µg/kg dose and when given acetylcholine. The responses to C4 and C5, while much less dramatic, were statistically significant at all dose levels.

Figure 26G

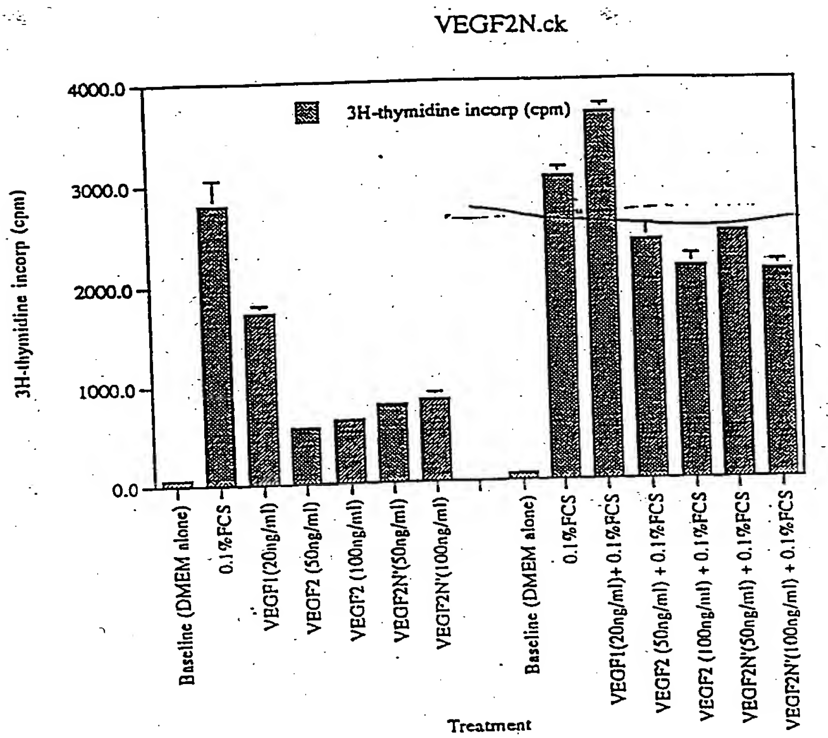


Figure 27

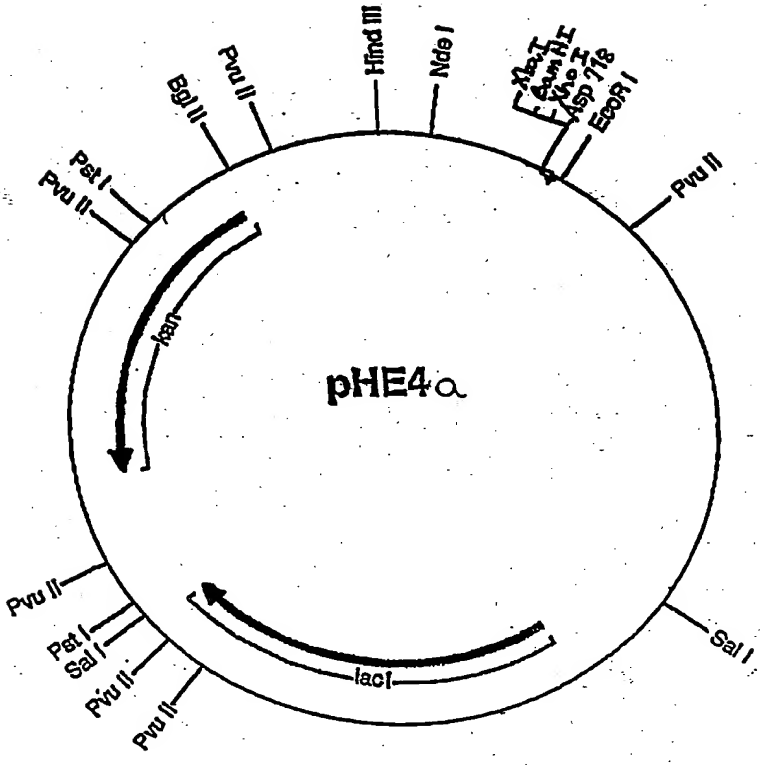


Figure 28

Figure 29